

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/563,270  
Source: IFWP  
Date Processed by STIC: 1/13/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/563,270

TIME: 10:16:00

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01132006\J563270.raw

5 <110> APPLICANT: Monsanto Technology LLC  
 7 Baum, James A.  
 8 Donovan, Judith C.  
 10 Donovan, William P.  
 12 Engleman, James T.  
 14 Krasomil-Osterfeld, Karina  
 16 Pitkin, John W.  
 18 Roberts, James K.  
 22 <120> TITLE OF INVENTION: Insecticidal Proteins Secreted From Bacillus Thuringiensis  
 and Uses  
 23 Therefor  
 27 <130> FILE REFERENCE: 38-21(52806)B  
 C--> 30 <140> CURRENT APPLICATION NUMBER: US/10/563,270  
 C--> 30 <141> CURRENT FILING DATE: 2006-01-04  
 30 <150> PRIOR APPLICATION NUMBER: PCT/US04/21692  
 32 <151> PRIOR FILING DATE: 2004-07-06  
 35 <150> PRIOR APPLICATION NUMBER: US 60/485,483  
 37 <151> PRIOR FILING DATE: 2003-07-07  
 41 <160> NUMBER OF SEQ ID NOS: 33  
 45 <170> SOFTWARE: PatentIn version 3.1  
 49 <210> SEQ ID NO: 1  
 51 <211> LENGTH: 15  
 53 <212> TYPE: PRT  
 55 <213> ORGANISM: Bacillus thuringiensis  
 59 <400> SEQUENCE: 1  
 61 Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Arg Val Gln Asp  
 62 1 5 10 15  
 65 <210> SEQ ID NO: 2  
 67 <211> LENGTH: 45  
 69 <212> TYPE: DNA  
 71 <213> ORGANISM: Artificial Sequence  
 75 <220> FEATURE:  
 77 <223> OTHER INFORMATION: tic gene probe encoding SEQ ID NO 1  
 79 <400> SEQUENCE: 2  
 80 gtaattggac catatgcaga atcatatatt gatacgagta caaga 45  
 83 <210> SEQ ID NO: 3  
 85 <211> LENGTH: 1253  
 87 <212> TYPE: DNA  
 89 <213> ORGANISM: Bacillus thuringiensis  
 93 <220> FEATURE:  
 95 <221> NAME/KEY: CDS  
 97 <222> LOCATION: (153)..(1253)  
 99 <223> OTHER INFORMATION:  
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104 aattatgatt ttaatatctct tatgttattc ctataatata caataaaagc ataattatcc      60
106 ttcataattat gtttataaat ttaataaaat acataaaaaat agagtgttat aatatttttg    120
108 aaagcgttat caagagtgat ggaggggataa tt atg aaa aat aga ttt tca aaa      173
109                                     Met Lys Asn Arg Phe Ser Lys
110                                     1                               5
112 gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt      221
113 Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser
114          10                               15                               20
116 tca agc atg tca gct ttt gct gca gaa gcc aaa tca cca gat tta aat      269
117 Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn
118          25                               30                               35
120 gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att      317
121 Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
122 40                               45                               50                               55
124 gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt      365
125 Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly
126          60                               65                               70
128 aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct      413
129 Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala
130          75                               80                               85
132 aga ttt tgg ata ttt aag gat caa aac aat aac cat cag aca aat aga      461
133 Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His Gln Thr Asn Arg
134          90                               95                               100
136 ttt ata tcc tgg ttt aaa gat aat att gct agt tca aaa ggg tat aat      509
137 Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys Gly Tyr Asn
138          105                               110                               115
140 agt att gcg gag caa atg ggt tta aaa ata gaa gca gaa aac gat atg      557
141 Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu Asn Asp Met
142 120                               125                               130                               135
144 gat gta aca aat ata gat tat aca tct aag aca ggc gat acc att tat      605
145 Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr
146          140                               145                               150
148 aat ggt att tca gaa ttg aaa aat tat aca gga tca act caa aag atg      653
149 Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr Gln Lys Met
150          155                               160                               165
152 aaa aca gat agt ttt caa aga gat tat aca aaa tca gaa tct act tca      701
153 Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu Ser Thr Ser
154          170                               175                               180
156 gta act aat gga tta caa tta gga ttt aaa gtt gct gct aaa gga gta      749
157 Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala Lys Gly Val
158          185                               190                               195
160 gtt gct ttg gct ggg gca gac ttt gaa acc agt gtt act tat aat cta      797
161 Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr Tyr Asn Leu
162 200                               205                               210                               215
164 tca act act aca act gaa aca aat aca ata tca gac aag ttt act gtc      845
165 Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val
166          220                               225                               230
168 cca tct caa gaa gtt aca ttg cct cca gga cat aaa gcg ata gtg aaa      893
169 Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala Ile Val Lys

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170          235          240          245
172 cat gat tta aga aaa atg gtt tat tct ggt act cat gat cta aag ggt      941
173 His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly
174          250          255          260
176 gat tta att gtg agt ttt aat gat aaa gag att gta caa aaa ttt att      989
177 Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile Val Gln Lys Phe Ile
178          265          270          275
180 tat cca aat tat aga gaa att aat tta tct gat atc cgt gaa act atg      1037
181 Tyr Pro Asn Tyr Arg Glu Ile Asn Leu Ser Asp Ile Arg Glu Thr Met
182 280          285          290          295
184 att gaa att gat gaa tgg aat cat gta aac cct gtg aat ttt tat gaa      1085
185 Ile Glu Ile Asp Glu Trp Asn His Val Asn Pro Val Asn Phe Tyr Glu
186          300          305          310
188 tta gtt ggg gtc aaa aat cat ata aaa aat ggt gaa act ttg tat ata      1133
189 Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Glu Thr Leu Tyr Ile
190          315          320          325
192 gat act cca gct aaa ttt atg ttt aat ggt gct aat cca tat tat aga      1181
193 Asp Thr Pro Ala Lys Phe Met Phe Asn Gly Ala Asn Pro Tyr Tyr Arg
194          330          335          340
196 gca aca ttt aca gaa tac gac ggg aat aat aat cct gtt caa aca aag      1229
197 Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Asn Pro Val Gln Thr Lys
198          345          350          355
200 gta tta agt gaa aac ttt aaa ttg      1253
201 Val Leu Ser Glu Asn Phe Lys Leu
202 360          365
205 <210> SEQ ID NO: 4
207 <211> LENGTH: 367
209 <212> TYPE: PRT
211 <213> ORGANISM: Bacillus thuringiensis
215 <400> SEQUENCE: 4
217 Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
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221 Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
222          20          25          30
225 Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
226          35          40          45
229 Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
230          50          55          60
233 Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
234 65          70          75          80
237 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
238          85          90          95
241 Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
242          100          105          110
245 Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
246          115          120          125
249 Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
250          130          135          140
253 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr

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254 145          150          155          160
257 Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
258          165          170          175
261 Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
262          180          185          190
265 Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
266          195          200          205
269 Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
270          210          215          220
273 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
274 225          230          235          240
277 Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
278          245          250          255
281 Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
282          260          265          270
285 Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu
286          275          280          285
289 Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
290          290          295          300
293 Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
294 305          310          315          320
297 Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
298          325          330          335
301 Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
302          340          345          350
305 Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
306          355          360          365
309 <210> SEQ ID NO: 5
311 <211> LENGTH: 1621
313 <212> TYPE: DNA
315 <213> ORGANISM: Bacillus thuringiensis
319 <220> FEATURE:
321 <221> NAME/KEY: CDS
323 <222> LOCATION: (530)..(1621)
325 <223> OTHER INFORMATION:

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332 tccaatgtgt gcctttctat atcaatcgca cgatataaat aacactatctt ccctttgaat 120
334 tttatatagg tttcatctaa ttttcaagac atgtggttgt tttgcgtttt cttcttccaa 180
336 atttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact 240
338 gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata 300
340 tcttgtttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgctttttt 360
342 tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa 420
344 accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgaatg 480
346 tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac 538
347                                     Met Lys Tyr
348                                     1
350 aag ttt tca aaa gtc gtt aag tgt act tta cca gct tta atg att act 586
351 Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr

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352	5	10	15	
354	aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg	634		
355	Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser			
356	20	25	30	35
358	cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct	682		
359	Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser			
360		40	45	50
362	tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca	730		
363	Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser			
364		55	60	65
366	aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga	778		
367	Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly			
368		70	75	80
370	tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat	826		
371	Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His			
372		85	90	95
374	caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg	874		
375	Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Ser			
376	100	105	110	115
378	aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca	922		
379	Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala			
380		120	125	130
382	tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt	970		
383	Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly			
384		135	140	145
386	gat acc ata tat aat gga att tct gaa cta aca aat tat aca gga aca	1018		
387	Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr			
388		150	155	160
390	acc caa aaa atg aaa acc gat agt ttt caa aga gat tat aca aaa tct	1066		
391	Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser			
392		165	170	175
394	gaa tcc act tca gta aca aat ggg tta caa tta gga ttt aaa gtt gct	1114		
395	Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala			
396	180	185	190	195
398	gct aag gga gta gtt gca tta gca ggt gca gat ttt gaa aca agt gtt	1162		
399	Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val			
400		200	205	210
402	acc tat aat tta tca tct act aca act gaa aca aat aca ata tcg gat	1210		
403	Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp			
404		215	220	225
406	aag ttt act gtt cca tct caa gaa gtt aca tta tcc cca gga cat aaa	1258		
407	Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro Gly His Lys			
408		230	235	240
410	gca gtg gtg aaa cat gat ttg aga aaa atg gtg tat ttt ggg act cat	1306		
411	Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe Gly Thr His			
412		245	250	255
414	gat tta aag ggt gat tta aaa gta ggt ttt aat gat aaa gag att gta	1354		
415	Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val			
416	260	265	270	275

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:26; N Pos. 3,9  
Seq#:27; N Pos. 6,24  
Seq#:28; N Pos. 6  
Seq#:29; N Pos. 18

**VERIFICATION SUMMARY**

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Input Set : A:\pto.da.txt

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L:30 M:270 C: Current Application Number differs, Replaced Current Application No  
L:30 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:103 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:99  
L:329 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:325  
L:567 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:563  
L:803 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:799  
L:1080 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1076  
L:1451 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1473 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1495 M:259 W: Allowed number of lines exceeded, <223> Other Information:  
L:1539 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
L:1578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0  
L:1607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0  
L:1636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0  
L:1659 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:1655